

## TTIC 31050 # 1

### 1

I completed this task in python. I only have the final alignments of the benchmark sequences in my file, but it was tested on several shorter sequences.

### 2

Unfortunately the sequence I have selected has some similar strings along it, which appear to be fooling my implementations. I'm scoring 0% accurate in both cases, which is due to the gaps in my implementation not appearing in the same places as the ground truth.

### 3

My local alignment is successfully identifying 100% identical subsequences, unfortunately they don't appear in the same places along the two sequences resulting in a score of 0. As stated above my global alignment is also not performing very well.

### 4

Due to the already 0 scores for my implementations, changing to an affine gap penalty doesn't have a quantitative effect on the alignment score. However, a manual examination shows what we would expect. Increasing the penalty to open gaps decreases the number of gaps, increasing the penalty to keep a gap open decreasing the lengths of the gaps present.